

B

		% of GFP positive cells			
		Med	IL-4	CD40	IL-4+CD40
XF-1		0.5+0.2	1.0+0.3	1.9+0.2	2.7 ± 0.3 (3)
XF-5a		0.7+0.2	2.8+0.4	3.2+0.3	54.3 ± 5.4 (4)
XF-8		0.3+0.1	0.3+0.2	1.5+0.2	7.6 ± 2.3 (8)
XF-2b		0.8+0.3	0.9+0.2	2.8+0.3	3.1 ± 0.6 (4)
XF-2a		0.7+0.2	1.2+0.3	3.2+0.2	3.6 ± 0.7 (3)
XF-6a		0.9+0.3	2.9+0.3	3.8+0.5	28.6 ± 4.2 (4)
XF-6b		0.6+0.2	0.8+0.2	1.2+0.2	3.7 ± 0.7 (3)
XA-1					

FIGURE 1

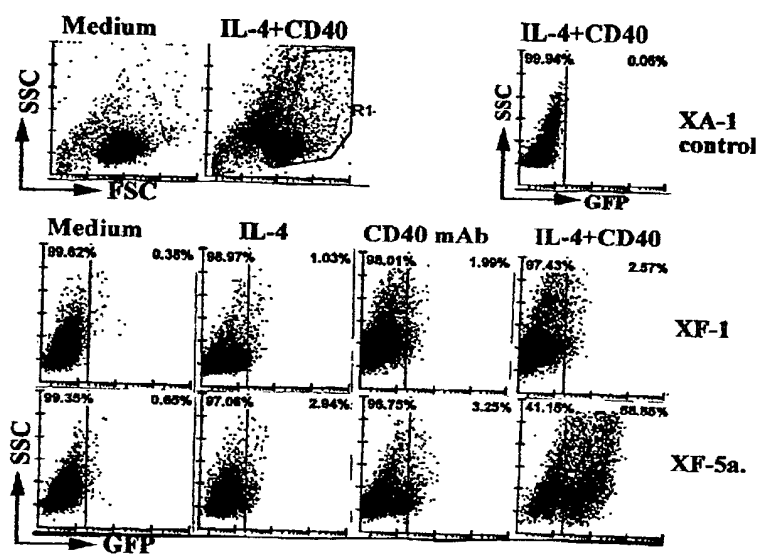


FIGURE 2

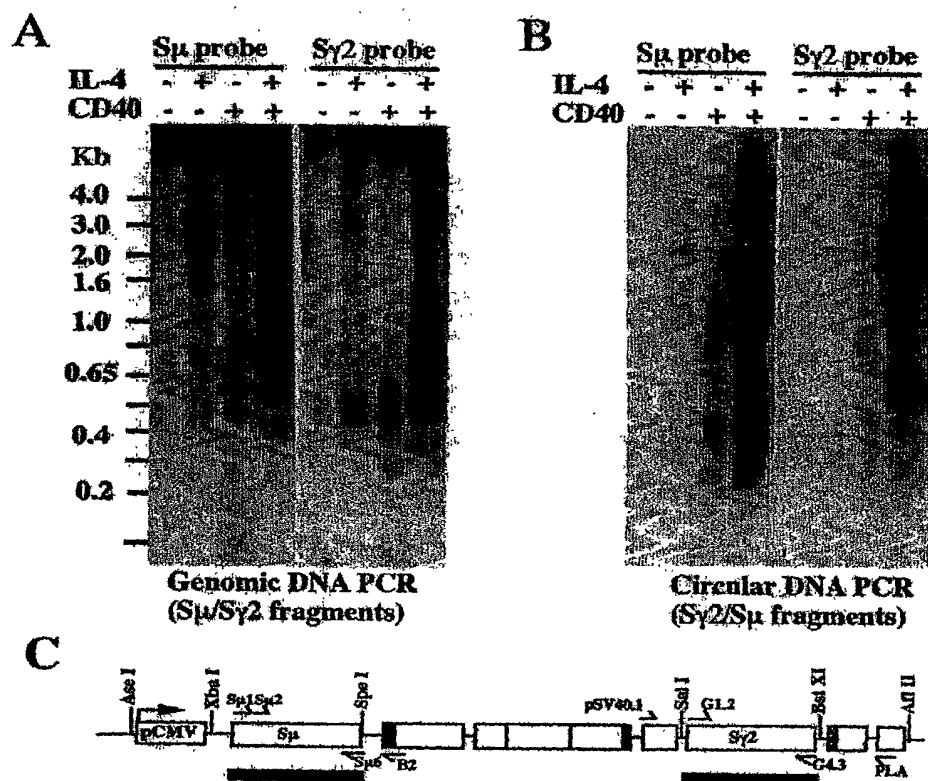


FIGURE 3

A

Sp	TTGGCTTCACTGGGCTTGGCTTGGCTTGGCTTGAAGGGGTC 577	Sp	TTTACTTGGCTTCACTGACTCACTTCACTTGGCTTGAAG 652
15-15	TTGGCTTCACTGGGCTTGGCTTGAAGGCTTGAAGCTTGAAGG	16-16	TTTCACTTGGCTTCACTTGAAGCTTGAAGCTTGAAGCTTGAAG
Sp2	CAGCCACAGTTCAGGAGGCTTGGCTTGAAGCTTGAAGCTTGAAG 2292	Sp2	CGTTTCACTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 1263
Sp	CTAACGCTCTTCACTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 409	Sp	TGGCTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 597
41-44	CTAACGCTCTTCACTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT	41-27	TGGCTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT
Sp2	TCACTTCACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1454	Sp2	GGCTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 2512

...

B

Sp2	AAGGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1510	Sp2	CAGGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1061
38-41	AAGGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT	38-45	CAGGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT
Sp	CTAAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 617	Sp	TGGCTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1455
Sp2	CTAAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1103	Sp2	TCAAGCTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1237
39-42	CTAAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	38-48	TCAAGCTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT
Sp	TGGCTTGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1506	Sp	AAGGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1396

C

Sp	CGTGGCTTGGCTTGAAGCTTGGCTTGAAGCTTGGCTTGAAGCT 639	Sp	TGAAGCTTGGCTTGGCTTGGCTTGGCTTGAAGCTTGGCTTGGCTTGGCT 562
40-43	CGTGGCTTGGCTTGAAGCTTGGCTTGAAGCTTGGCTTGAAGCT	40-45	TGAAGCTTGGCTTGGCTTGGCTTGGCTTGAAGCTTGGCTTGGCTTGGCT
CD2	TCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 821	CD2	TCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 914

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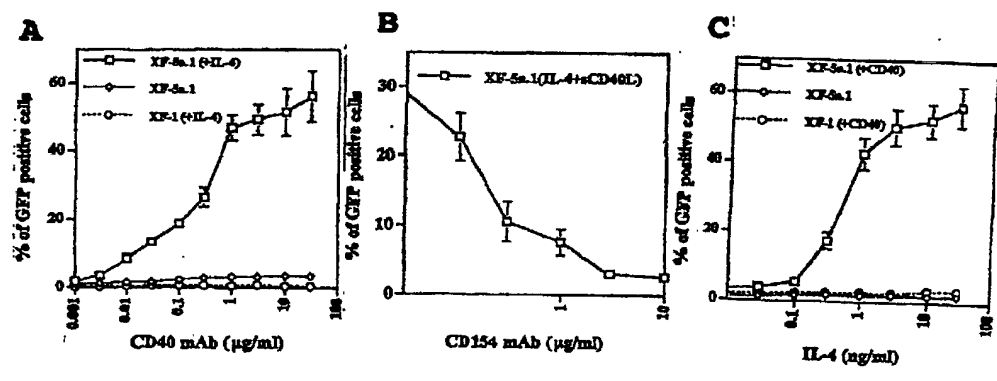


FIGURE 5

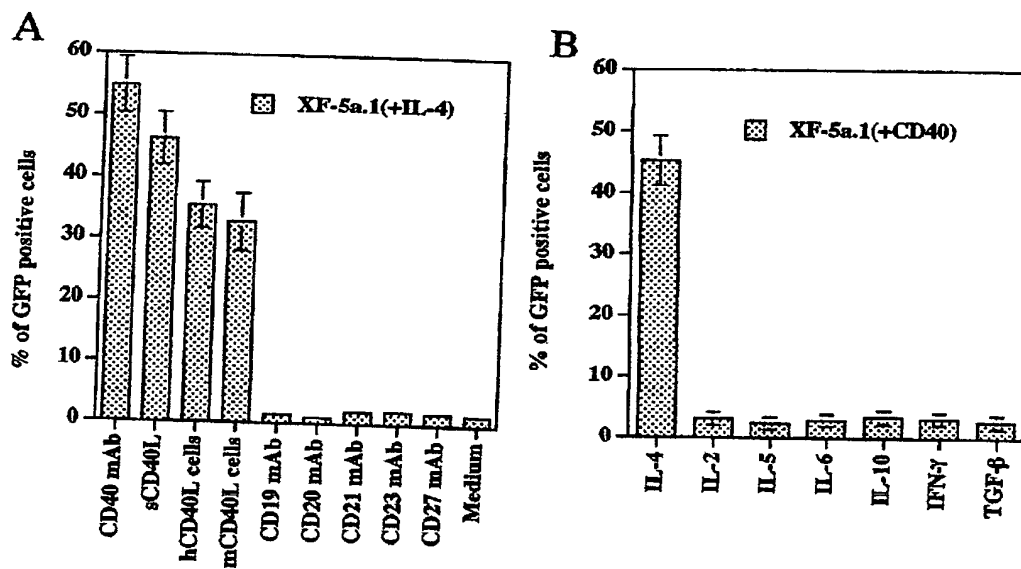


FIGURE 6

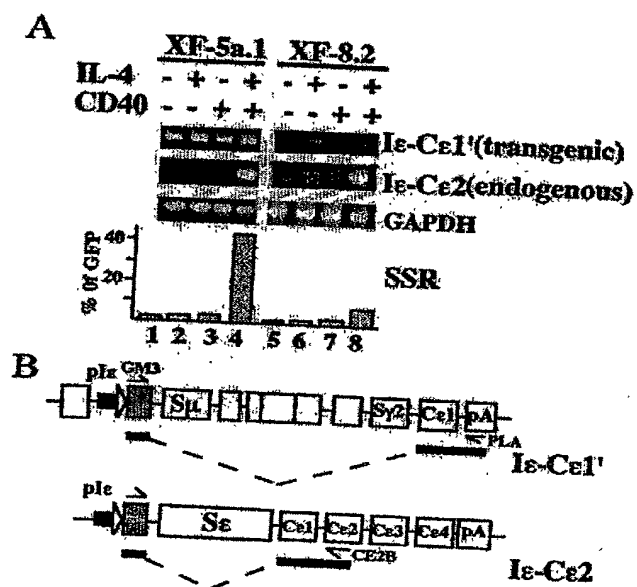
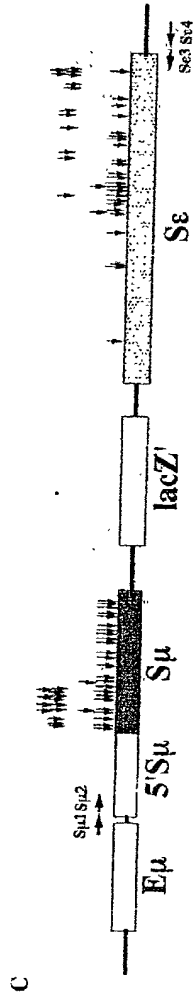


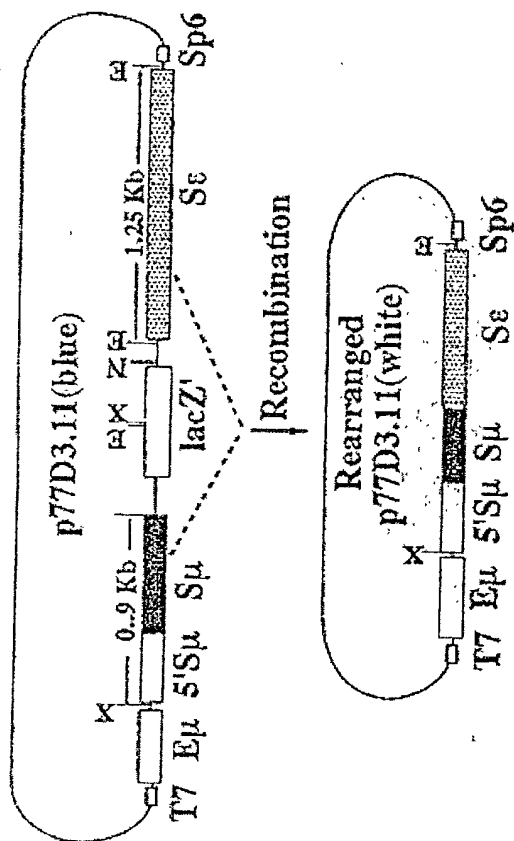
FIGURE 7

FIGURE 7
(CONTINUED)



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FIGURE 8



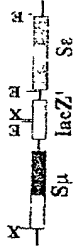
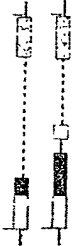
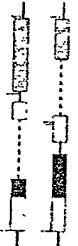
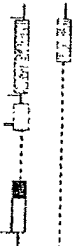
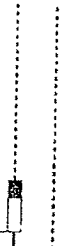





Recombination models	Mapping fragments by X+E	Colony analyzed	Ratio (%)
	3		
	1	269	87.6%
	1	ND	ND
	2	3	1.0%
	2	3	1.0%
	3	3	1.0%
	0 (linearized)		
	0 (linearized)	8	2.6%
	0 (linearized)		
	0 (supercoiled)	21	6.8%
Total		307	100%

FIGURE 9

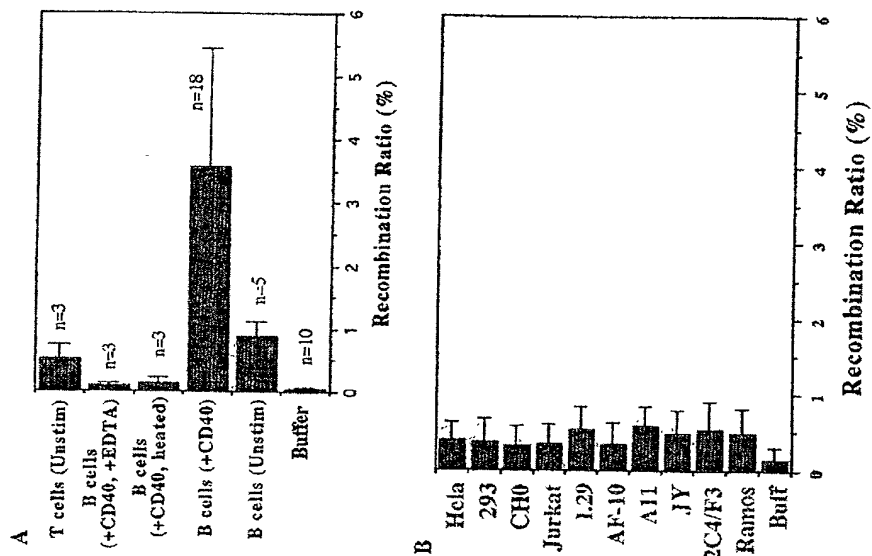


FIGURE 10

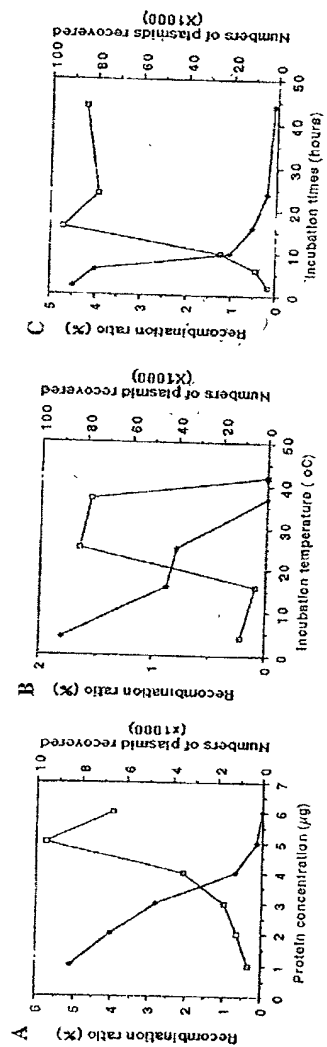


FIGURE 11

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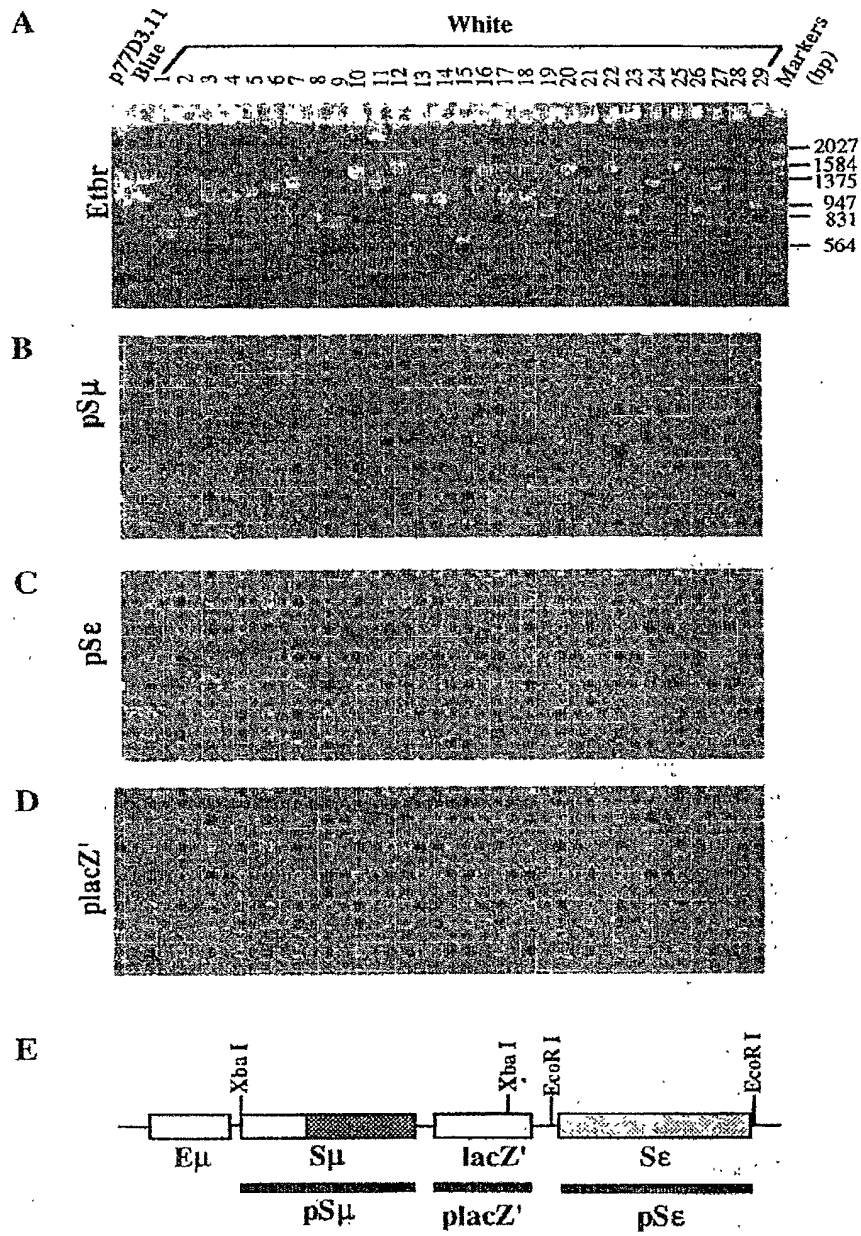


FIGURE 12

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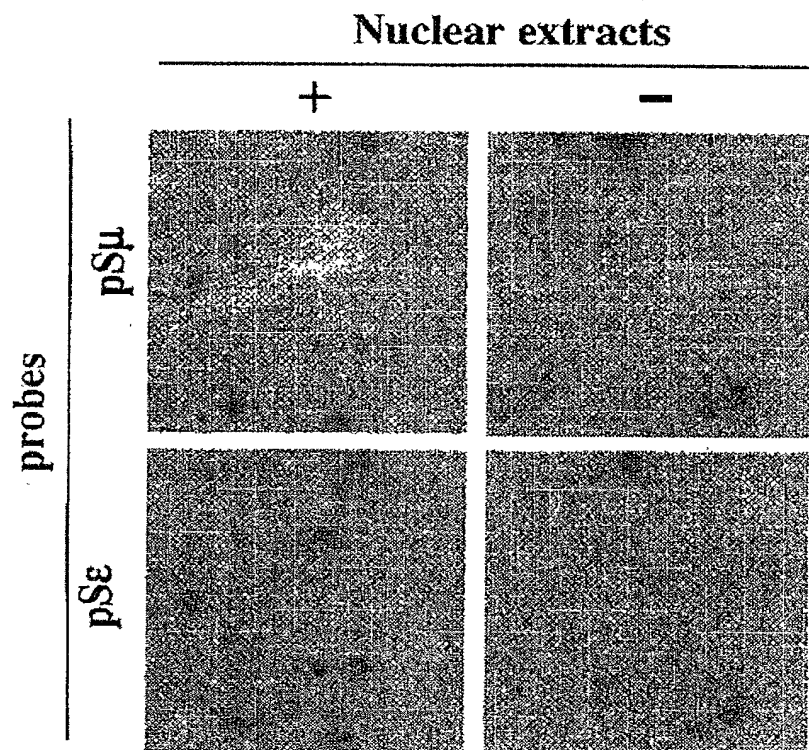


FIGURE 13

